

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/451,939DATE: 12/19/1999  
TIME: 04:18:14

INPUT SET: S34265.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANTS: Miao, Ningning  
Wang, Monica  
Mahanthappa, Nagesh K.  
Jin, Ping  
Pang, Kevin

(ii) TITLE OF INVENTION: Method of Treating Dopaminergic and  
GABA-nergic Disorders

(iii) NUMBER OF SEQUENCES: 22

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
(B) STREET: ONE POST OFFICE SQUARE  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02109

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII (text)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/900,220  
(B) FILING DATE: 24-JUL-1997

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.  
(B) REGISTRATION NUMBER: 36,709  
(C) REFERENCE/DOCKET NUMBER: ONV-044.01

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000  
(B) TELEFAX: (617) 832-7000

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47
48
49 (2) INFORMATION FOR SEQ ID NO:1:
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 1277 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: both
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: cDNA
57
58 (ix) FEATURE:
59 (A) NAME/KEY: CDS
60 (B) LOCATION: 1..1275
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48
65 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
66 1 5 10 15
67
68 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC 96
69 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
70 20 25 30
71
72 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG 144
73 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
74 35 40 45
75
76 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA 192
77 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
78 50 55 60
79
80 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC 240
81 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
82 65 70 75 80
83
84 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA 288
85 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
86 85 90 95
87
88 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG 336
89 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
90 100 105 110
91
92 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC 384
93 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
94 115 120 125
95
96 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC 432
97 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
98 130 135 140
99

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100	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
101	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
102	145 150 155 160	
103		
104	TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC	528
105	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
106	165 170 175	
107		
108	TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC	576
109	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
110	180 185 190	
111		
112	TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG	624
113	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
114	195 200 205	
115		
116	CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG	672
117	His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
118	210 215 220	
119		
120	GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC	720
121	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
122	225 230 235 240	
123		
124	TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC	768
125	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
126	245 250 255	
127		
128	GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC	816
129	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
130	260 265 270	
131		
132	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG	864
133	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
134	275 280 285	
135		
136	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA	912
137	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
138	290 295 300	
139		
140	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT	960
141	Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
142	305 310 315 320	
143		
144	GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA	1008
145	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
146	325 330 335	
147		
148	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC	1056
149	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
150	340 345 350	
151		
152	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA	1104

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153 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
154          355                      360                      365
155
156 TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC      1152
157 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
158          370                      375                      380
159
160 ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG      1200
161 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
162          385                      390                      395                      400
163 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT      1248
164 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
165          405                      410                      415
166
167 CCG CTG GGC ATG GTG GCA CCG GCC AGC TG      1277
168 Pro Leu Gly Met Val Ala Pro Ala Ser
169          420                      425
170
171
172 (2) INFORMATION FOR SEQ ID NO:2:
173
174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 1190 base pairs
176 (B) TYPE: nucleic acid
177 (C) STRANDEDNESS: both
178 (D) TOPOLOGY: linear
179
180 (ii) MOLECULE TYPE: cDNA
181
182 (ix) FEATURE:
183 (A) NAME/KEY: CDS
184 (B) LOCATION: 1..1191
185
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
187
188 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG      48
189 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
190 1          5          10          15
191
192 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG      96
193 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
194          20          25          30
195
196 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT      144
197 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
198          35          40          45
199
200 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG      192
201 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
202          50          55          60
203
204 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC      240
205 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn

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	65	70	75	80	
206					
207					
208	TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC				288
209	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp				
210		85	90	95	
211					
212	CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC				336
213	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile				
214		100	105	110	
215					
216	GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC				384
217	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly				
218		115	120	125	
219					
220	TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC				432
221	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly				
222		130	135	140	
223					
224	CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT				480
225	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly				
226		145	150	155	160
227					
228	TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC				528
229	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr				
230		165	170	175	
231					
232	GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG				576
233	Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu				
234		180	185	190	
235					
236	GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG				624
237	Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu				
238		195	200	205	
239					
240	CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG				672
241	Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp				
242		210	215	220	
243					
244	GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG				720
245	Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu				
246		225	230	235	240
247					
248	CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG				768
249	Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val				
250		245	250	255	
25					

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/451,939**

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*INPUT SET: S34265.raw*

Line

Error

Original Text